506 754/80

Сору	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	
OM nucleic - nucleic search, using sw model	earch, using sw model	
Run on: April	April 11, 2006, 17:45:01 ; Search time 706.552 Seconds (without alignments) 11734.281 Million cell updates/sec	
Title: US-08-	US-08-939-905D-1	

Title:

WS-08-939-905D-1

Perfect score: 1244
Sequence: 1 atgggttccatgcgtctatt......ttaaggtacttaattaatca 1244
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100*
Maximum Match 100*
Listing first 100 summaries

Database: N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2001as:*
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10: geneseqn2003as:*
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13: geneseqn2004as:*
13: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2005s:

	Description	Aav30460 Soybean s	Aav59077 Soybean s	Aeb48290 Soybean s	Adt18491 Plant cDN	Aeb48312 Soybean s	Ada01016 cDNA enco	Aeb48299 Soybean s	Aav59078 Soybean s	Aeb48311 Soybean s	Aav30461 Soybean s	Aaz29902 Nucleotid	Aeb48291 Soybean B	Ada01015 Genomic D	Ada01019 Soybean D	Aeb48303 Medicado	Aeb48300 Medicado	Aeb48301 Medicado	Aeb48302 Medicado	Aac33558 Arabidops
SUMMARIES	ΩI	AAV30460	AAV59077	AEB48290	ADT18491	AEB48312	ADA01016	AEB48299	AAV59078	AEB48311	AAV30461	AAZ29902	AEB48291	ADA01015	ADA01019	AEB48303	AEB48300	AEB48301	AEB48302	AAC33558
	DB	7	7	14	13	14	σ	14	7	14	N	~	14	σ	σ	14	14	14	14	m
	Query Match Length DB	1244	1244	1244	1348	1200	1056	1031	3359	3359	4700	4700	4700	4655	4648	1200.	1200	1200	1200	1294
عِن	Query Match	100.0	100.0	100.0	100.0	96.5	84.9	74.0	53.8	53.8	53.8	53.8	53.8	50.2	49.3	45.2	43.0	42.8	41.1	29.5
	Score	1244	1244	1244	1244	1200	1056	920	699	699	699	699	699	624	613	562	534.4	532.4	511.2	363.2
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Add7027 Rice gene
Adj11381 Rice DNA
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	
OM nucleic - nucleic search, using sw model	
Run on: April 11, 2006, 17:48:45 ; Search time 6171.24 Seconds (without alignments) 11458.523 Million cell updates/sec	

1 atgggttccatgcgtctatt......ttaaggtacttaattaatca 1244 US-08-939-905D-1 1244 Title: Perfect score: Sequence:

AB193819 Pisum sat L36156 Medicago sa L36157 Medicago sa AF405327 Lupinus a X97351 P.trichocar AB087838 Pisum sat AF479623 Populus nig D30653 Populus nig D30653 Populus nig D30653 Populus kit X97350 P.trichocar AF0552 A.thaliana AY056186 Arabidops AJ247742 Ipomoca b AY0507019 Sequence

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

11766282 Total number of hits satisfying chosen parameters:

5883141 segs, 28421725653 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

gb_ba:*
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gb_or:* gb_gt;; gb_un; gb_vi;; gb_htg;; GenEmbl: * Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	L78163 Glycine max	AR351556 Sequence	U41657 Glycine max	L81148 Glycine max	BD244520 Seed coat	AF014502 Glycine m	AR351555 Sequence	AF149277 Phaseolus	AR351558 Sequence	AF007211 Glycine m	X90692 M.sativa mR	AF403735 Lupinus a	AB193818 Pisum sat	L36111 Stylosanthe	X90693 M.sativa mR	X90694 M.sativa mR	AB193817 Pisum sat	AB193820 Pisum sat
SUMMARIES	α	SOYCVH63A	AR351556	GMU41657	SOYCVH63SC	BD244520	AF014502	AR351555	AF149277	AR351558	AF007211	MSRNAPE1A	AF403735	AB193818	SSNPEROXIB	MSRNAPE1B	MSRNAPE1C	AB193817	AB193820
	DB	15	ø	15	15	9	15	9	15	9	15	15	15	15	15	15	15	15	15
	* Query Match Length DB	1244	1056	1031	3359	4700	4700	4655	1176	4648	1287	1220	1351	1199	1311	1238	1287	1246	1462
	Query Match	100.0	84.9	74.0	53.8	53.8	53.8	50.2	49.5	49.3	45.8	45.2	45.0	44.4	43.1	43.0	42.8	42.6	42.3
	Score	1244	1056	920	699	699	699	624	616.4	613	569.2	562	559.4	552.4	536.6	534.4	532.4	529.4	526.4
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J02979 Nicotiana t AR034949 Sequence 136779 Sequence 23 D0078754 Brassica AF324700 Arabidops AF452387 Arabidops

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AB193820 Pisum sat AB193819 Pisum sat AB007211 Glycine m X90693 M. sativa mR AB193817 Pisum sat AP405327 Lupinus a L36157 Medicago sa X97351 P. trichocar AP002032 Arabidops AJ742742 Ipomoea b D38050 Populus kit	AYE19359 Arabidops AYE19359 Arabidops AC149540 Populus t X99952 A.thaliana AY096186 Arabidops AY087674 Arabidops B83224 Populus nig B83225 Populus nig AX507019 Sequence AX651264 Sequence AX651264 Sequence AX651264 Sequence AX651269 P.trichocar AF488305 GOSSYplum AY519360 Arabidops AX507289 P.trichocar X97349 P.trichocar X97349 P.trichocar X877349 P.trichocar X8718877 Arabidops AX61273 Sequence AX61282 Populus kit AX599046 Sequence AX60463 Arabidops AX60381 Arabidops AX60381 Arabidops MS6381 Arabidops	BT001238 Arabidops AF452385 Arabidops AX099555 Arabidops AX012629 Sequence AX412629 Sequence AX412629 Sequence AX6921689 Sequence AX651689 Sequence AX651689 Sequence AX651689 Arabidops AF059106 Arabidops AF05938 Arabidops AF05938 Arabidops AF05938 Arabidops AF05938 Arabidops AF05938 Arabidops AF06768 Lotus cor M37157 A.rusticana D11396 Nicotiana AJ781007 Raphanus M5880 Arabidopsis AL13296 Arabidopsis AL13296 Arabidopsis AX081286 Sequence AF455807 Nicotiana X71591 L.esculentu AY423440 Brassica X19023 Lycopersico AY531529 Brassica AX599046 Sequence AX599046 Sequence
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leic -	Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq le Maximum DB seq le Post-processing: Database:	Result Score gree and is despected by the second of the se

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5.1.7 Biocceleration Ltd.		Search time 2669.45 Seconds (without alignments) 11734.281 Million cell updates/sec	ttaaggtacttaattaatca 4700			: 9993994								d by chance to have a the result being printed, re distribution.		Description	Aav30461 Soybean s Aaz29902 Nucleotid Aeb48291 Soybean s	Ada01015 Genomic D Ada01019 Soybean D Aeb48311 Soybean s	Aav59078 Soybean s Aeb48317 Soybean s	Aeb48319 Soybean B Aeb48319 Soybean B Dav30460 Soybean B	Aav59077 Soybean s Aeb48290 Soybean s	Adt18491 Plant CDN Aeb48312 Soybean s Aeb48299 Soybean s		
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Bioco	OM nucleic - nucleic search, using sw model	Run on: April 11, 2006, 17:45:01; Search (withou	Title: US-08-939-905D-2 Perfect score: 4700 Sequence: 1 tagataaaaaatgggatattt	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 4996997 seqs, 3332346308 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	Database : N Geneseq 21:* 1: geneseqn1980s:*	2: genesequiogous: 3: genesequ2000s:* 4: geneseqn2001as:* 5: geneseqn2001bs:*	ים נים נים נים	9: geneseqn2003bs:* 10: geneseqn2003cs:* 11: geneseqn2003ds:* 12: qeneseqn2004as:*	13: genesegn2004bs:* 14: genesegn2005s:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Score Match Length DB	4700 100.0 4700 2 4700 100.0 4700 2 4700 100.0 4700 14	4632.6 98.6 4655 9 4613.6 98.2 4648 9 3359 71.5 3359 14	3355.8 71.4 3359 1532 32.6 1532	1524 32.4 1524 14 1074 22.9 1074 14 669 14 2 1244 2	669 14.2 1244 669 14.2 1244	669 14.2 1348 13 625 13.3 1200 14 559 11.9 1031 14	2 4 4	

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.	using sw model	<pre>6, 17:55:53 ; Search time 17929.4 Seconds    (without alignments)    12264.715 Million cell updates/sec</pre>	D-2 atgggatatttaaggtacttaattaatca 4700	Gapext 1.0	, 23393541228 residues	ng chosen parameters: 82156650	0000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	: 100 summaries	•					results predicted by	to the score of the result of the total score distribut	SUMMARIES		B ID Descript.	BE822567 BE822567	BE822838 BE822838 AW277864	BE660610 BE660610	AW278026 AW278026	AW279469 AW279469 BE660615 BE660615	AI960823 AI960823	BE610364 BE6100364 BE61000364 BE61000364 BE61000000000000000000000000000000	AW705730 AW705730 AW705730	BE608629 BG653639 BG653639	AW706826 AW704798	AW596852 AW596852	1 AN278775 AN278775 SE97402.y 6 CA919442 CA919442 EST637160
Copyright (c	OM nucleic - nucleic search, u	Run on: April 11, 2006,	Title: US-08-939-905D-2 Perfect score: 4700 Sequence: 1 tagataaaaaatgggat	Scoring table: IDENTITY_NUC Gapop 10.0 , G	Searched: 41078325 segs,	Total number of hits satisfying	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match Maximum Match	Listing		3: 9b est3:* 4: 9b htt:* 5: 9b est4:*					score greater than or equal and is derived by analysis	***	Query	NO. SCOKE MACCH Length L	625 13.3 664	3 582 12.4 663 4 492 10.5 494	490 10.4 540	479.4 10.2 546	479 10.2 541 471.2 10.0 803	0 465.6 9.9 583	2 422.4 9.0 592	3 413.2 8.8 602 4 387 8.2 584	5 384.2 8.2 639 6 378.2 8.0 448	7 361.4 7.7 363 8 327 7.0 370	9 323 6.9 333 0 314 6.7 342	304.8 6.5 632

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BO122725
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